

## **Leotiomyces updated 2022**

### **P.R. Johnston, October 2022, v40.5.pdf**

This unpublished phylogeny is based on the same set of genes used by Johnston et al. (2019) and uses the same methods. The 2019 dataset has been expanded to include additional genomes (some still unpublished) and isolates representing new genera and families, where multi-gene data are available. Some of this data (and some of the informal names used) are unpublished.

The file was prepared using an A0 format, so printing a readable version will be difficult.

The specimen labels include voucher specimen information, the genes available for each specimen, and usually an indication of family-level classification. The coloured clades mostly represent named families, the family names are provided as part of the specimen label text.

'v40.5\_family level summary.pdf' provides a summary at the family level that can be printed as A4.

The 'v40.5 source of data' spreadsheet provides voucher specimen details, GenBank accession numbers (where the data is not unpublished), and NCBI or JGI genome accessions for the taxa treated.

The earlier 2020 and 2021 versions of this analysis were trees v31\_6\_2.pdf and v40.pdf.

The 2022 analysis includes several additional genomes and multigene datasets, including several genera in Phacidiaceae.

Some comments on the October 2022 analysis results

- *Cadophora* sensu stricto (vascular staining pathogens, see Maciá-Vicente et al. 2020, <https://doi.org/10.1186/s43008-020-00036-w>) has a strongly supported sister relationship to *Drepanopezizaceae*, and collectively these two clades are monophyletic. Lifestyle differs between the clades (leaf spots versus vascular pathogens), so perhaps not taxonomically useful to include *Cadophora* in *Drepanopezizaceae*. The '*Cadophora*' species in *Ploettnerulaceae* are mostly associated with healthy roots.
- *Crocicreas gramineum* is strongly supported as sister to *Leptodontidiaceae*, but there is no particular ecological or morphological support for including *Crocicreas* in this family.
- *Mollisiaceae* and sister families have been treated in the sense of Tanney & Seifert (2020, <https://doi.org/10.1016/j.simyco.2020.02.005>)
- the large, poorly supported clade in *Helotiales* that contains specimens referred to *Vandijckellaceae*, Han et al. 2014 clade 9, *Calloria*, and the *Stamnaria* lineage sensu Baral 2016, shows little internal resolution and remains problematic.
- The *Helotiales* clade containing isolates referred to clade 3 by Han et al. (2014), appears to be phylogenetically distinct from both *Pezizellaceae* and *Hamatocanthoscyphaceae*, and perhaps deserves a name of its own. This clade includes several mostly unnamed New Zealand species associated with copious subiculum hyphae or clypeus-like covering layers and was discussed in more detail by Johnston (2020 - <https://datastore.landcareresearch.co.nz/dataset/austropezia-in-pezizellaceae-s-l/resource/edd331d9-4e17-415c-8908-4ac305e93eb3>)
- *Chalara* is polyphyletic, this morphology evolving independently several times – to resolve this, the type species needs epitypifying.

- New unpublished genomes for *Asperopilum juncicola* (PDD 99993) and a species morphological typical of *Lachnum* (PDD 93687) suggest *Asperopilum* is a synonym of *Lachnum*, despite being morphologically divergent.
- The well supported *Rhytismatales* clade includes several families with poorly defined relationships.
- *Thelebolales*, with additional sampling of *Pseudeurotiaceae*, contains three well-resolved clades — *Pseudeurotiaceae*, *Thelebolaceae* and *Holwayaceae*.

### **Leotiomyces updated 2021**

**P.R. Johnston, July 2021, v40.pdf**

A few comments on this analysis:

- the addition of several taxa at the base of the *Helotiales* (*Arachnoscypha*, a genome for *Xylogone*) phylogenetically close to *Polydesmia* seems to have stabilised relationships in this part of the tree.
- genomes from several additional taxa are treated for *Sclerotiniaceae*. The *Monilinia* clades 'Disjunctoriae' and 'Junctoriae' here have a sister relationship, the larger inclusive clade also monophyletic. rDNA based analyses generally show these taxa as two distinct clades distant within *Sclerotiniaceae* – the relationship shown in the analysis presented here could reflect a problem with the rDNA analyses, or could be due to inadequate taxon sampling.
- resolving *Mollisiaceae*, *Vibrisseaceae* and *Loramycetaceae* phylogenetically as separate families remains problematic.
- newly available data for *Cyttaria* places *Cyttariaceae* within *Helotiales*. In this analysis there is a sister relationship with *Chlorociboriaceae* but this position is unstable and dependent on the taxa sampled across *Helotiales*.
- the position of *Neolauriomycetaceae* is unstable, requiring additional genes and/or additional close taxa to resolve its position more reliably. Other analyses have placed it isolated within *Helotiales*, and in this case there is a strongly supported sister relationship between *Erysiphaceae* and *Arachnopezizaceae*.
- *Urceolella* is poorly sampled genetically and its position needs confirming with additional genes.
- the large, poorly supported clade in *Helotiales* that contains specimens referred to *Vandijkellaceae*, Han et al. 2014 clade 9, *Calloria*, and the *Stamnaria* lineage sensu Baral 2016, shows little internal resolution and remains problematic.
- The *Helotiales* clade containing isolates referred to clade 3 by Han et al. (2014), appears to be phylogenetically distinct from both *Pezizellaceae* and *Hamatocanthoscyphaceae*, and perhaps deserves a name of its own. This clade includes several mostly unnamed New Zealand species associated with copious subiculum hyphae or clypeus-like covering layers and was discussed in more detail by Johnston (2020 - <https://datastore.landcareresearch.co.nz/dataset/austropezia-in-pezizellaceae-s-l/resource/edd331d9-4e17-415c-8908-4ac305e93eb3>)
- Relationships of genera such as *Claussenomyces* and *Aotearoamyces* within *Leotiales* remain poorly resolved.

Baral H-O (2016) Inoperculate discomycetes. pp 157–205. In: Jaklitsch W, Baral H-O, Lücking R, Lumbsch HT, Frey W (eds) Syllabus of plant families: A. Engler's syllabus der Pflanzenfamilien part 1/2. Borntraeger, Stuttgart, p 322

Han JG, Hosoya T, Sung GH, Shin HD (2014) Phylogenetic reassessment of *Hyaloscyphaceae* (sensu lato *Helotiales*, *Leotiomyces*) based on multigene analyses. *Fungal Biology* 118: 150–167.

Johnston PR, Quijada L, Smith CA, Baral HO, Hosoya T, Baschien C, Pärtel K, Zhuang WY, Haelewaters D, Park D, Carl S, López-Giráldez F, Wang Z, Townsend JP (2019) A multigene phylogeny toward a new phylogenetic classification for the *Leotiomyces*. *IMA Fungus* 10 (1):1-22.